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Integration of GWAS and brain transcriptomic analyses in a multi-ethnic sample of 35,245 older adults identifies DCDC2 gene as predictor of episodic memory maintenance

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1. NARRATIVE

1.1 Contextual background

As we age, our cognitive abilities deteriorate [1], without necessarily progressing to dementia. One of the earliest and most striking cognitive changes in the aging process is the alteration of memory. Episodic memory, our ability to remember recently acquired

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experiences gradually deteriorates from middle age to older age. Our ability to create and storage memories (encoding and storage) along with its retrieval [2] becomes less efficient, interfering with our daily activities.

Major research efforts have focused on trying to distinguish the memory decline attributable to normal aging from those that indicate pathological aging. Such studies shown that the effects of aging in our memory performance are very heterogeneous, with clear inter-individual vulnerabilities. Some people exhibit little change in their memory ability to extreme old age, while others experience a rapid and severe memory decline that might culminate in a clinical diagnosis of Alzheimer's disease. Understanding the causal factors underlying over-time memory performance is increasingly important given the health care crisis of an aging world's population. Psychological, health-related, environmental, education and genetics [3] factors have been reported as significant contributors to the variability observed in the trajectories of episodic performance across individuals.

Twin and family studies support the notion that episodic memory is under strong genetic influence in older persons in healthy and demented populations[4]. In recent years, different study designs and approaches have been used to genetically characterize episodic memory trajectories. The majority of the genetic studies on episodic memory have been cross-sectional either using genome-wide arrays [5–7] or candidate genes approaches [8–18]. Genetic studies based on longitudinal measures of episodic memory are few, and predominantly focused on candidate genes [19, 20]. Genome-wide association studies (GWAS) of cognitive abilities assessing the contribution of common variants [11, 17, 18, 21–29] have consistently reported modest genetic effects, partly due to limited sample sizes that compromise the statistical power to identify loci at a genome-wide significance level. As reported for other complex phenotypes [30, 31], such as autoimmune and cardiovascular diseases, genomic analysis including rare variants might reveal its unique roles in cognitive genetics.

In the present study, we integrated common and rare genetic variants and transcriptomics data for the identification of novel episodic memory loci.

1.2 Study design and main results

To guarantee a better understanding of the impacts of ageing, cohort differences and period effects in the trajectories of memory performance, we considered a longitudinal study design.

The identification of genetic risk/protective factors underlying memory function are commonly based on cross-sectional data and genetic studies based on longitudinal data are less frequently implemented. Contrary to cross-sectional designs in which a temporal sequence cannot be established, longitudinal methods are uniquely able to capture genetic variation associated with the rate of cognitive decline [32], allowing the separation of population trends (fixed effects) and individual differences about the trends (random effects). The availability of longitudinal measures of memory performance allow us to expand genetic analyses beyond the dichotomous case-control phenotype, typically resulting in loss of measurement information as well as effect size and statistical power.

To study trajectories of memory performance in elderly cohorts, we have used a previously described latent curve models approach (LCM) [33]. The resulting slopes of repeated measures of memory are used as quantitative phenotype for genetic analyses [32].

Since GWAS common variants explain a modest fraction of the genetic variance of cognitive abilities [25], low-frequency and rare genetic variants have been proposed as responsible for the uncharacterized genetic risk underlying cognitive traits [30]. A cost-efficient approach to characterize the contribution of rare variants to memory function is their genotype imputation, that is, statistically inference of untyped rare variants' genotypes based on a reference panel of whole genome sequenced individuals [34]. The publically available Haplotype Reference Panel (HRC) reference panel contains over 39 million SNPs from 27,165 individuals, and reported high performance and accuracy for imputation for admixed populations such as African-Americans [35] and Caribbean Hispanics [36].

In addition to the traditional SNP-based approaches [37], we have also considered gene-based GWAS association tests. Gene-based analyses increases the statistical power of discovery by i) aggregating the disparate signals from multiple independent causal variants within the gene and ii) by reducing the multiple testing burden (~1,000,000 million SNPs versus ~20,000 genes). Moreover, since the impact of genetic heterogeneity due to underlying linkage disequilibrium patterns (different SNPs being linked to the causal variants) is reduced when considering the gene as the unit of analysis, it can alleviate limitations in replication leading to more consistent results [38].

In an attempt to improve our understanding of the genetic architecture of memory function, our study has included participants from ethnically diverse populations: Caribbean Hispanics and African-Americans. A disproportionate majority of participants in cognitive genetics research are of European descent. However, it is well established that the effect of genetic variants vary between populations based on the reported differences in the genetic architecture of populations [39]. Moreover, low-frequency and rare variants tend to be ethnic specific (i.e. exhibit little sharing among diverged populations) and enriched in admixed populations[40]. The inclusion of multi-ancestry cohorts in genetics studies are needed to fully characterize human genomic variation, bolster our understanding of disease etiology, and ensure that genetic testing is broadly accessible.

Results from *APOE*-stratified GWAS analyses and brain transcriptomics identified Doublecortin Domain Containing 2 gene (*DCDC2*) as a novel predictor of memory maintenance among non-carriers of *APOE*-ε4. *DCDC2* brain expression appeared associated with episodic memory maintenance and lower burden of pathological Alzheimer's hallmarks. Moreover, when AD cases were compared to cognitively healthy participants, *DCDC2* expression was decreased across all brain areas.

1.3 Study conclusions, disease implications, and therapeutic opportunities

Our multi-omics data integrative approach using meta-analysis results from eight independent GWAS of episodic memory trajectories and brain transcriptomics for three independent cohorts identified *DCDC2* as a putative gene for protection against episodic memory decline and a potential to reduce risk of dementia.

To our knowledge, this is the first study reporting *DCDC2* association with longitudinal changes in episodic memory performance. Interestingly, the *DCDC2* gene was previously reported as genome-wide significantly associated with general cognitive function ($p < 5 \times 10^{-8}$) in a sample of more than 300,000 subjects from three different European cohorts including UKBB [25].

The DCX domain-containing protein 2 (*DCDC2*) gene is one of the most conserved genes of the doublecortin (DCX) superfamily, a group of proteins that regulate filamentous actin structure in developing neurons. *DCDC2* binds to tubulin and enhances microtubule polymerization [41, 42] influencing synaptic plasticity [43]. It is well documented that cytoskeleton dynamics in the adult brain affect fundamental processes, such as memory and learning, which are often compromised in neuro degenerative diseases [44, 45]. In fact, genetically modified mice studies showed that *DCDC2* mutations resulted in persistent memory impairments [46, 47]. Multiple epidemiological genetic studies linked variants within *DCDC2* gene to reading abilities including dyslexia [48–55]. A recent re-evaluation suggested that evidence in support of the *DCDC2* deletion as a risk factor for dyslexia was statistically weak [56]. Our results in the Non-Hispanic White sample of the WHICAP cohort did not find significant association between *DCDC2* and language trajectories.

Reinforcing its role in brain development, *DCDC2* has also been found to interact with ciliary proteins. Ciliary proteins play an important role in neurogenesis, neuronal migration, and underlie a growing list of human disorders including developmental delays and cognitive deficits. Protein–protein interaction network analysis[57] revealed a link between cilia function, neuronal function, and neurological disorders such as Alzheimer's disease. These results provide a novel therapeutic avenue in which drugs targeting proteins in the cilia interactome might be repurposed for treating neurological disorders.

The inverse association between brain expression levels and lower amyloid and tau pathology may selectively upregulate *DCDC2* expression in the dorsolateral prefrontal cortex, conferring protection against Alzheimer's pathology. Follow-up studies are needed to determine whether reserve mechanisms (brain reserve [58, 59], cognitive reserve [58, 59] and brain maintenance [59, 60]) might act as moderators.

Our results found differential brain expression of *DCDC2* when AD cases and cognitively healthy participants were compared. Specifically, gene expression in AD cases appeared nominally downregulated for two brain areas, superior temporal gyrus (temporal lobe), and inferior frontal gyrus (prefrontal cortex). Future studies incorporating neuroimaging data will be needed to validate these results and gain a better understanding of its neuroanatomical correlates.

The identification of *DCDC2* gene as a predictor of memory maintenance in older adulthood provides the possibility of identifying population subgroups at-risk of memory decline and dementia, paving the way for precision medicine intervention [32, 61–63]. Compared to the universal "one-size-fits-all" approach (generalized prevention strategies for all individuals), a precision medicine approach offers the opportunity to personalize interventions that hold the promise of advancing memory decline prevention strategies [64]. To be used as a

diagnostic system and more efficient treatment of age-related memory impairment it will require i) to define groups of individuals for whom a cognitive intervention is warranted and ii) to develop and test novel treatments and interventions that can be applied with a degree of specificity to distinct subpopulations of individuals[65]. Finally, it is important to consider that relying solely on genetics may miss unknown underlying memory decline mechanisms. In addition to genetics, a precision medicine approach should also encompass recommendations to target lifestyle factors and medical comorbidities on an individual basis.

1.4 Limitations, unanswered questions, and future directions

Our study has some limitations. First, trajectories of episodic memory were modelled as a linear function of time, hence we did not consider potential nonlinear age effects. Second, we did not consider the contribution of additional protective or/and risk factors, socio-economic status, mental or behavioral health, and clinical comorbid conditions that may be associated with maintenance/decline of memory. Third, potential interactions between genetic variants and these risk/resilience additional factors may also contribute to set courses toward memory progression over time. Fourth, we cannot rule out the possibility that additional regulatory mechanisms might regulate *DCDC2* expression variation.

Future translational studies will investigate the role of *DCDC2* variants in cytoskeleton dynamics via generation of CRISPR-pluripotent cellular models expressing different variants of *DCDC2* gene and differentiated into neurons (cortical or hippocampal). Cytoskeleton structure and organelle distribution can be assessed by confocal imaging using these cell models. Furthermore, expression of proteins involved in posttranslational modifications of microtubules, such as acetylation can be also investigated by western blot and qPCR analysis.

2. Consolidated description of methods and results

Using latent class models, we have estimated episodic memory trajectories in 35,245 ethnically diverse older adults representing eight independent cohorts. We conducted *APOE*-stratified GWAS analyses and combined individual cohorts ‘results via meta-analysis. Three independent transcriptomics datasets were used to further interpret GWAS signals.

We identified *DCDC2* gene significantly associated with episodic memory ($P_{meta}=3.3 \times 10^{-8}$) among non-carriers of *APOE*-ε4. Brain transcriptomics revealed an association between episodic memory maintenance and i) increased dorsolateral prefrontal cortex *DCDC2* expression ($p=3.8 \times 10^{-4}$) and ii) lower burden of pathological Alzheimer’s hallmarks (PHF-tau p=0.003, and amyloid-beta load p=0.008). Additional transcriptomics results comparing Alzheimer’s disease and cognitively healthy brain samples showed a downregulation of *DCDC2* levels in superior temporal gyrus (p=0.007) and inferior frontal gyrus (p=0.013).

3. Complete methods and results

3.1 Methods

Study Cohorts.—All study participants provided written informed consent and the study procedures were approved by the Institutional Review Boards within each of the corresponding institutions. All study procedures were performed in accordance with the World Medical Association Declaration of Helsinki ethical principles for medical research.

The present study includes eight independent study cohorts: 1) The Alzheimer's Disease Genetics Consortium and National Alzheimer's Coordinating Center (ADGC_NACC), 2) The National Institute on Aging Late-Onset Alzheimer Disease Family Based Study (NIA-LOAD), 3) The Chicago Health and Aging Project (CHAP), 4) The Religious Orders Study and Rush Memory and Aging Project (ROSMAP), 5) The Washington Heights-Inwood Columbia Aging Project (WHICAP), 6) The Long Life Family Study (LLFS), 7) The Alzheimer's Disease Neuroimaging Initiative (ADNI) and the 8) United Kingdom Biobank (UKBB). Detailed characteristics and methodologies for study cohorts can be found elsewhere [33, 66–68].

Within each of the study cohorts, inclusion criteria for participants were based on the availability of longitudinal episodic memory scores (minimum of two visits to a maximum of 15), socio-demographic variables (sex, age, education and ethnic background), and imputed GWAS genotyped data using the Haplotype Reference Consortium (HRC v1.1).

An overview of the study design is summarized in Supplemental Figure 1.

Episodic memory.—In the WHICAP cohort, episodic memory was derived as the average of standardized measures for total immediate recall, delayed recall, and delayed recognition of the Selective Reminding Tests [69]. In the ADNI cohort, the Rey Auditory Verbal Learning Test (RAVLT) [27, 70] served as a measure of episodic memory. In the UKBB, as previously described [23], participants' scores on the pairs matching test can be used as a measure of episodic visual memory. As previously described [33], in the rest of cohorts, episodic memory was quantified as the average of the standardized Wechsler Memory Scale tests.

Alzheimer's disease.—In all study cohorts, except for LLFS and UKBB, participants were classified as dementia patients or non-cognitively impaired (NCI) participants using NINCDS-ADRDA) criteria [71]. In the LLFS cohort, dementia status was categorized based on a previously described diagnostic algorithm [72]. In the UKBB cohort, cognitive impairment was defined using a 1.5-SD cut-off below demographically adjusted episodic memory scores (age, education, and sex). UKBB study participants were classified as non-cognitive impaired (NCI) if their standardized adjusted memory scores were greater than 1.5 SD below the mean.

Statistical Analysis

Statistical analyses were performed using a dataset freeze from 2019 for which complete and accurate phenotypic and genomic information was available.

Episodic memory trajectories (EMTs).—As previously described [33], episodic memory trajectories were derived using Latent Class Mixed Models (LCMM). The LCMM estimated episodic memory slope was used as quantitative outcome.

Genome-wide genotype (GWAS) imputation.—Genome-wide genotyped data was imputed using the Haplotype Reference Consortium panel (HRC v1.1) through the Michigan Imputation online server [73].

Quality control metrics.—Samples were excluded for analyses purposes based on: cryptic relatedness (duplicates or first degree relatives) calculated as identity by descent estimates using PLINK [74] software, and genotype call missing rate greater than 10%. Only variants with high imputation quality ($r^2 \geq 0.8$) were retained for analyses purposes.

Population substructure.—To account for population stratification, principal component analysis was conducted using PLINK software [74] and the top three principal components were retained as covariates in regression models.

Gene-based association analyses.—Gene-based annotations were generated using ANNOVAR software [75] and were limited to intronic, exonic, 3' and 5' untranslated regions variants. Analyses were conducted only for genes with at least 10 annotated variants. Gene-based test were run using the optimal single-nucleotide polymorphism–set Sequence Kernel Association Test (SKAT-O) as implemented in EPACTS [76]. Covariates in the linear regression models included sex, age at last evaluation, education and the top three principal components. For LLFS cohort, further covariates adjustment included kinship correlation matrix. All analyses were conducted independently in three different *APOE* strata: no *APOE* stratification, *APOE-ε4* carriers vs. non-carriers. Gene-level significance was established as $p \leq 2.7 \times 10^{-6}$ after Bonferroni's correction for multiple testing (an average of 20,000 genes annotated across all cohorts).

SNP-based and gene-based meta-analysis.—Meta-analysis of the gene-based and SNP-based association results was carried out using inverse variance–weighted model based on p-values/sample size and metrics to measure between-study heterogeneity (Cochran's Q-test)[77] as implemented in METAL software [78]. Using Bonferroni for multiple testing correction, a conservative threshold for significance was set as $p \leq 2.5 \times 10^{-6}$ and $p \leq 1.6 \times 10^{-4}$ for gene-based and SNP-based respectively).

DCDC2 SNP-based analyses in APOE-ε4 non-carriers.—Variants in *DCDC2* gene were individually tested for its association with episodic memory using EPACTS software. Sex, age at last evaluation, education, principal components, and kinship matrix (only for the LLFS cohort) were included as covariates in the model. SNP-level significance was established as $p \leq 1.5 \times 10^{-5}$ after Bonferroni's correction for multiple testing based on the total number of SNPs tested in the meta-analysis.

SNP-based APOE interaction analyses.—The regression-based approach implemented in the epistasis module of PLINK [74] was used to run test pair-wise

interactions between the strongest *DCDC2* associated variant in the SNP-based meta-analysis (rs1340698) and *APOE* genotype, carriers and non-carries of *APOE-ε4*.

Brain transcriptomic analyses.—RNA sequencing data processed in the present study can be accessed on the Accelerating Medicines Partnership- Alzheimer's Disease (AMP-AD) Synapse knowledge portal (https://www.synapse.org). The AMP-AD is a public-private partnership focused on the development of new drug targets to prevent or treat Alzheimer's disease. The threshold for nominal significance was defined as P-values ≤0.05.

Brain transcriptomic analysis Religious Orders Study and Rush Memory and Aging Project (ROSMAP) study.—RNA sequencing (RNA-seq) data generated by ROSMAP [79–82] consisted of post-mortem dorsolateral prefrontal cortex (DLPFC) brain tissue from 624 participants (254 syndromic Alzheimer's disease, 169 mild cognitive impairment and 201 no cognitive impairment).

Brain transcriptomic analysis in The Mount Sinai Brain Bank (MSBB) study.—The MSBB analyses included a total of 476 samples collected from four different brain areas: parahippocampal gyrus (PHG), inferior frontal gyrus (IFG), superior temporal gyrus (STG) and the frontal pole FP (n=476). Detailed specific sample characteristics and methodological pipeline can be found elsewhere [83].

Brain transcriptomic analysis in the Mayo clinic dataset.—The analyses of the Mayo RNA-seq dataset included samples harvested from temporal cortex and cerebellum. Detailed specific sample characteristics and methodological pipeline can be found elsewhere [84].

Summary data-based Mendelian Randomization (SMR).—We used a Mendelian Randomization approach to investigate whether *DCDC2* variants associated with episodic memory performance could act through *DCDC2* gene expression levels in brain. eQTLs analyses were performed using SMR software [85]. Because of the lack of publically available episodic memory GWAS summary statistics, we relied on SNP-based association results from the largest cohort in our study, UKBB cohort (*DCDC2*_noE4 strata, n= 14,874). Reference eQTL data were obtained from the Brain-eMeta dataset, which includes brain tissue eQTL data from GTEx v6, the CommonMind Consortium (CMC), ROS/MAP, and the Brain eQTL Almanac project (Braineac). The linkage disequilibrium (LD) estimation was based on the entire UKBB sample (n= 20,184). Software and reference database details can be accessed at https://cnsgenomics.com/software/smr/#SMR&HEIDIanalysis.

DCDC2 patterns of linkage disequilibrium (LD).—We investigated the linkage disequilibrium pattern between most significant associated SNPs in the Mendelian randomization analyses (topSMR) and *DCDC2* topSNPs in the GWAS meta-analysis (noE4 SNP-based association strata). All LD analyses were performed using NIH web-based application LDlink (LD matrix module) (https://ldlink.nci.nih.gov/?tab=home) (Myers, 2020).

DCDC2 and APOE interaction.—Gene-gene interaction was tested using epistasis module of PLINK [74].

3.2 Results

The characteristics of the participants within each are summarized in Table 1. A higher percentage of women was observed across all cohorts. The average age (at baseline and at last evaluations) and education of the participants were 72 ± 8, 78 ± 8 and 14 ± 3, respectively. The majority of the participants across cohorts were non-carriers of the *APOE-ε4* allele, and as expected, lower frequency of dementia when compared to *APOE-ε4* carriers.

Episodic memory trajectories.—Within study cohorts' trajectories of episodic memory are shown in Supplemental Figure 2. Consistent with previous literature, the majority of the participants were aggregated into the $EMT_{Stables}$ cluster (individuals exhibiting sustained or improved memory function over time). LCMM plots could not be generated for the LLFS cohort because, as described in the methods section, a different regression framework was used.

Meta-analysis of genomewide gene-based test of association.—The quantile-quantile plots for the gene-based association results within each of the cohorts stratify by *APOE* status are shown in Supplemental Figures 3–5. The average's statistics for SNP allele frequencies (minimum, maximum, average and standard deviation) stratify by study's cohort are shown in Supplemental Table 1. In the non-*APOE* stratified sample, the meta-analysis results (Table 2) revealed the doublecortin domain-containing family member (*DCDC2*) gene as the strongest association signal ($P_{meta}= 3.7 \times 10^{-7}$). More interestingly, the *DCDC2*-EM association was significant stronger among non-*APOE*-ε4 study participants ($P_{meta}=3.3 \times 10^{-8}$). Additional potential novel loci were observed in both *APOE* strata, however, none of the associations reached the same significance level as *DCDC2*. Secondary analyses excluding the UKBB cohort (Supplemental Table 2) corroborated that associations reported (Table 2) were not solely driven by the largest cohort in the study.

Meta-analysis of DCDC2 single-SNP association in the non-carriers of the APOE-ε4.—A total 1,144 variants in *DCDC2* appeared to be present in all study cohorts. The results from the SNP-based meta-analysis are summarized in Table 3, and study's regional association plots are shown in Figure 1. The strongest SNP-based association corresponded to intronic common SNP rs1340698 ($P_{meta}=1.3 \times 10^{-7}$). As seen in Supplemental Figure 6, the strong regional LD block ($r^2 \geq 0.6$) included the top-associated SNP rs1340698. The top SNP is located in the vicinity of a weak neuronal enhancer that connects to one of the two *DCDC2* promoters. However, nor the SNP or the LD block yielded significant eQTL effects in standard datasets (GTEx, GRASP).

DCDC2 and APOE interaction.—The results from epistatic models (Table 4) revealed that there is no significant interaction between the strongest *DCDC2* associated variant in the SNP-based meta-analysis (rs1340698) and *APOE* genotype.

Brain transcriptome results.—ROSMAP results (Table 5) revealed FDR-adjusted association between episodic memory maintenance and increased *DCDC2* expression in dorsolateral prefrontal cortex ($p=3.8 \times 10^{-4}$). When evaluating additional ROSMAP neuropathological traits, the increased *DCDC2* expression levels were associated with: Tau protein (measured as the average cortical density of antibodies to abnormally phosphorylated Tau in eight brain regions, p=0.003), overall amyloid beta level (measured as the average of the percent area that is occupied by amyloid beta in eight different brain regions, p=0.008), neurofibrillary tangle burden (measured as the average of tangle count in silver-stained slides from 5 regions, p=0.009), neuritic plaque burden (measured as the average of neuritic plaque count in silver-stained slides from 5 regions, p=0.011) and global burden of Alzheimer's disease pathology (measured as the average of counts in three pathologies: neurofibrillary tangles, neuritic and diffuse plaques in silver-stained slides from 5 regions, p=0.012).

Differential brain expression results from MSBB and Mayo datasets (Figure 2) revealed an overall decreased *DCDC2* expression (across all brain areas when AD cases were compared to controls. *DCDC2* downregulated expression achieved nominally statistical significance (~2-fold change, $p<0.05$) in two specific brain areas: superior temporal gyrus (p=0.007) and inferior frontal gyrus (p=0.013).

Mendelian randomization results identified common variant rs12216513 as significant eQTL for *DCDC2* expression (B=0.29, SE=0.04, $p=1.1 \times 10^{-11}$). This *DCDC2* variant is in tight LD with meta-analysis topSNPs, common (rs1340698, D'=0.88) and rare (rs147661578, D'=0.84). However, the effect of *DCDC2* variants on episodic memory performance over-time is not mediated by its brain expression (SMR p-value=0.950) (Supplemental Figure 7).

Because the widely reported association of *DCDC2* with phonological awareness and phonemic decoding [86], secondary analyses in WHICAP tested the *DCDC2* association with LCMM estimated trajectories of language [87]. The gene-based association results indicated no significant association between *DCDC2* and decay of language in none of the *APOE* strata considered (Supplementary Figure 8).

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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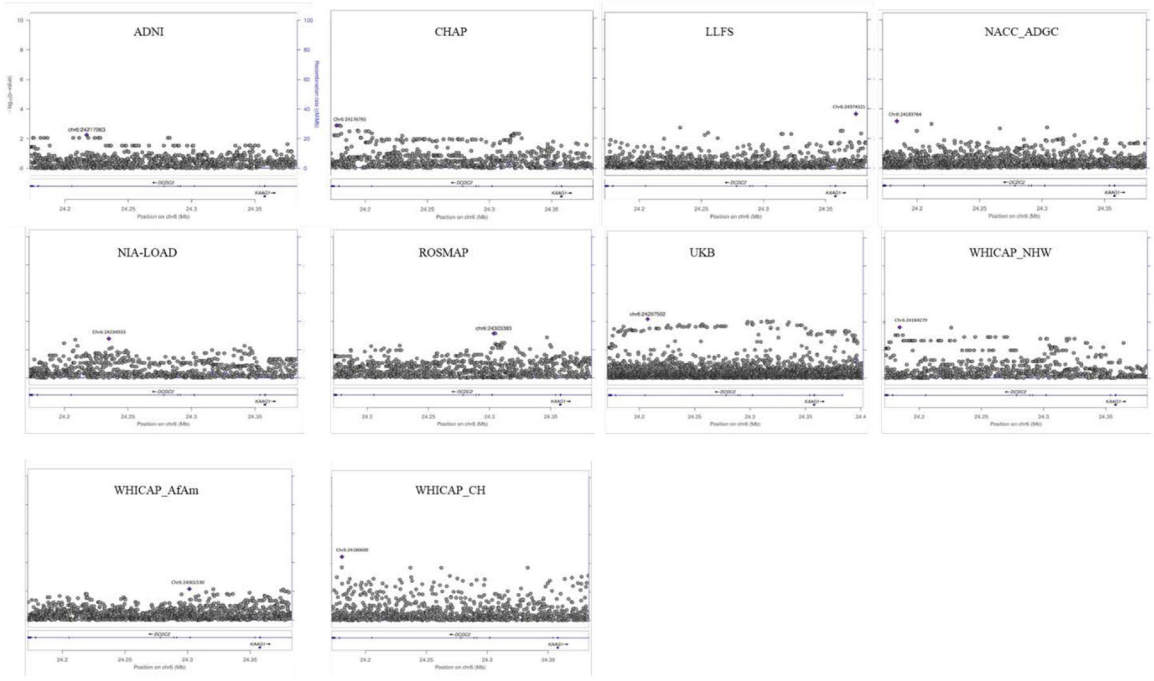

Figure 1.

Regional association plots for SNP based *DCDC2* analysis in the *APOE*-noE4 strata. The X-axis represent the GRCh37/hg19 chromosomal position (Mb) of the tested SNP variant(s); the left Y-axis correspond to the statistical strength of the SNP association (log10 (p value)). The right y-axis displays the estimated recombination rates (cM/Mb) to reflect the local LD structure. NHW: Non-Hispanic Whites; AfAm: African-Americans; CH: Caribbean-Hispanics.

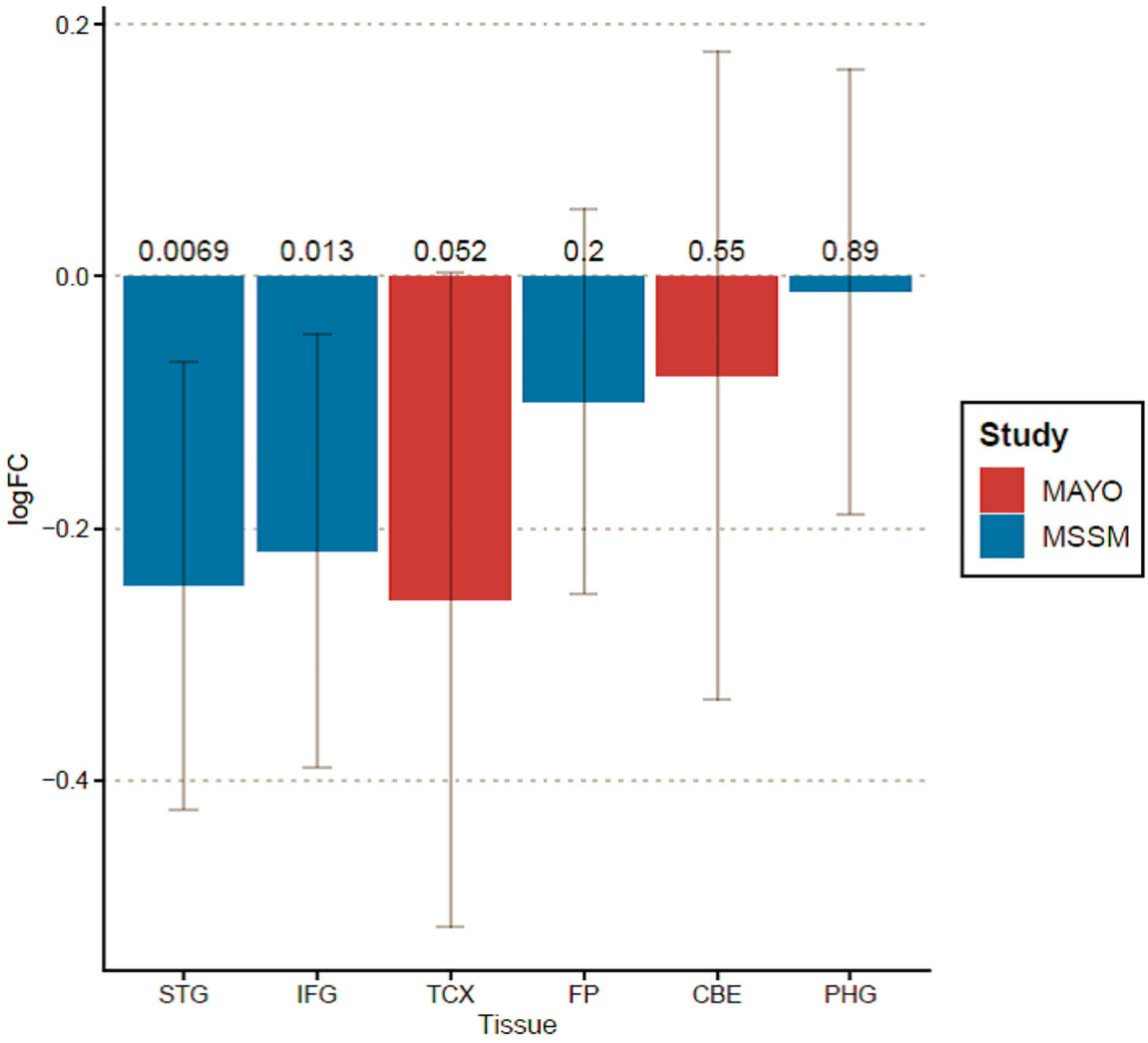

Figure 2.

DCDC2 brain transcriptome results from Mount Sinai Brain Bank (MSBB) and Mayo Clinic datasets.

The X-axis represents the brain regions analyzed from each cohort: Mount Sinai Brain Bank: superior temporal gyrus (STG), inferior frontal gyrus (IFG), frontal pole (FP), and parahippocampal gyrus (PHG); Mayo Clinic: temporal cortex (TCX) and cerebellum (CBE). The Y-axis correspond to the estimated tissue-specific fold change in DCDC2 expression (in red upregulation, in blue downregulation) and the 95% confidence intervals.

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Table 1.

Characteristics of the study participants by cohort.

	N	women		age_{BA}	age_{LE}	educ	$EMT_{Stables}$		$EMT_{Decliners}$		dem_{BA}		$non\text{-}dem_{BA}$		*APOE*_e4		*APOE*_none4	
		n	%				n	%	n	%	n	%	n	%	n	%	n	%
ADNI	1,090	634	58	74±7	79±8	16±3	380	35	710	65	322	30	768	70	501	46	589	54
CHAP	696	431	62	72±5	82±6	15±3	362	52	334	48	10	1	686	99	165	24	531	76
LLFS	1,874	1,040	55	64±11	71±11	12±3	1,047	56	827	44	131	7	1,743	93	400	21	1,474	79
NACC_ADGC	6,774	3,845	57	74±9	78±9	16±3	4,014	59	2,760	41	3,016	44	3,758	55	2,731	40	4,043	60
NIA-LOAD	460	298	65	73±9	77±8	16±3	253	55	207	45	31	7	429	93	152	34	308	64
ROSMAP	1,265	883	70	79±8	87±7	16±4	651	51	614	49	952	75	313	25	317	25	948	75
UKBB	20,184	10,322	51	55±8	63±7	91%	17,451	86	2,733	14	1,390	7	18,794	93	5,310	26	14,874	74
WNHW	619	370	60	76±7	80±8	13±4	597	93	22	7	45	7	574	93	121	19	498	81
WAA	736	532	72	75±6	79±7	12±4	712	97	24	3	37	5	699	95	244	33	492	67
WCH	1,547	1,093	71	76±6	81±7	7±4	972	61	614	39	561	35	1,025	65	402	25	1,184	75

EMTs: Episodic Memory Trajectories; age_{BA}: age at baseline evaluation; age_{LE}: age at last evaluation; dem_{BA}: dementia status at baseline evaluation; non-demBA: non-dementia status at baseline evaluation; WNHW: WHICAP Non-Hispanic Whites; WAA: WHICAP African-Americans; WCH: WHICAP Caribbean-Hispanics

Table 2.

Top significant genes ($p \leq 10^{-6}$) in the genome-wide gene-based meta-analysis stratify by *APOE* status.

		Meta-analysis			ADNI		CHAP		LLFS		NACC		NIA-LOAD		ROSMAP		UKBB		WNHW		WAA		WCH	
	Chr_Gene	**N**	**P_{meta}**	**P_{Het}**	**N**	**P**	**N**	**P**	**N**	**P**	**N**	**P**	**N**	**P**	**N**	**P**	**N**	**P**	**N**	**P**	**N**	**P**	**N**	**P**
no*APOE*	6_*DCDC2*	35,250	3.3E-07	0.204	1,090	0.377	696	0.741	1,874	0.030	6,774	0.473	460	0.536	1,265	0.006	20,184	6.7E-04	619	0.953	736	0.732	1,547	0.002
	16_*FBXL19*	35,245	4.5E-06	0.208	1,090	0.384	696	0.278	1,874	0.667	6,774	0.048	460	0.029	1,265	0.093	20,184	0.018	619	0.280	736	0.506	1,547	3.5E-04
	15_*ICE2*	35,245	2.8E-06	0.262	1,090	0.780	696	0.294	1,874	0.854	6,774	0.006	460	0.703	1,265	0.016	20,184	0.006	619	0.318	736	0.001	1,547	0.434
	17_*KRT37*	35,245	9.0E-06	0.445	1,090	0.034	696	0.066	1,874	0.550	6,774	0.605	460	0.298	1,265	0.352	20,184	8.5E-04	619	1.000	736	0.567	1,547	0.275
	16_*MTHFSD*	35,245	8.3E-06	0.769	1,090	0.504	696	0.188	1,874	0.299	6,774	0.850	460	0.308	1,265	0.430	20,184	1.7E-04	619	0.417	736	0.115	1,547	0.085
	16_*NPRL3*	35,245	9.5E-06	0.642	1,090	0.323	696	0.787	1,874	0.334	6,774	0.000	460	0.140	1,265	0.207	20,184	0.041	619	0.805	736	0.219	1,547	0.659
	11_*OR4C45*	35,245	6.6E-06	0.834	1,090	0.735	696	0.066	1,874	0.638	6,774	0.005	460	0.495	1,265	0.069	20,184	0.008	619	0.933	736	0.588	1,547	0.476
*APOE*_e4	6_*AKAP12*	10,333	2.8E-06	0.815	502	0.003	165	0.445	400	0.110	2731	0.059	152	1.000	316	0.753	5,310	0.001	121	1.000	241	0.486	395	0.436
	16_*ANXA11*	10,332	6.1E-06	0.421	501	0.043	165	0.548	400	0.589	2731	0.140	152	0.076	316	0.106	5,310	0.007	121	0.091	241	0.894	395	0.009
	15_*FIBP*	10,332	8.6E-06	0.962	501	0.844	165	0.273	400	0.336	2731	0.122	152	0.326	316	0.077	5,310	0.000	121	0.994	241	0.336	395	0.374
	17_*KBTBD12*	10,332	5.6E-06	0.809	501	0.009	165	0.751	400	0.379	2731	0.003	152	0.561	316	0.793	5,310	0.019	121	0.740	241	0.859	395	0.077
	16_*KIT*	10,332	2.3E-06	0.952	501	0.454	165	0.037	400	0.160	2731	0.046	152	0.459	316	0.481	5,310	0.001	121	0.355	241	0.194	395	0.378
	16_*L3MBTL3*	10,333	2.9E-06	0.946	502	0.193	165	0.432	400	0.179	2731	0.001	152	0.697	316	0.051	5,310	0.018	121	0.671	241	0.737	395	0.334
	11_*MERTK*	10,332	3.9E-06	0.304	501	0.002	165	0.062	400	0.024	2731	0.246	152	0.138	316	0.293	5,310	0.006	121	0.347	241	0.584	395	0.392
	6_*PADI4*	10,332	9.6E-06	0.407	501	0.291	165	0.412	400	0.509	2731	0.026	152	0.158	316	0.042	5,310	0.050	121	0.591	241	0.011	395	0.024
	10_*SUCLG1*	10,332	6.5E-06	0.103	501	0.253	165	0.131	400	0.492	2731	1.000	152	0.249	316	0.370	5,310	3.0E-05	121	1.000	241	0.001	395	0.472
*APOE*_noe4	6_*DCDC2*	24,913	3.4E-08	0.284	593	0.087	531	0.351	1474	0.038	4043	0.307	308	0.400	948	0.010	14,874	5.3E-04	498	0.003	492	0.181	1152	0.132
	16_*MTHFSD*	24,909	7.8E-07	0.560	589	0.100	531	0.212	1474	0.046	4043	1.000	308	0.112	948	0.778	14,874	4.1E-05	498	0.248	492	0.330	1152	0.140
	15_*ARSK*	24,909	2.5E-06	0.937	589	0.849	531	1.000	1474	0.270	4043	0.002	308	0.881	948	0.824	14,874	2.0E-04	498	0.897	492	0.261	1152	0.705
	17_*RALGDS*	24,909	3.9E-06	0.986	589	0.415	531	0.286	1474	0.578	4043	0.061	308	0.816	948	0.629	14,874	3.1E-04	498	0.062	492	0.443	1152	0.444
	16_*CYP2W1*	24,909	6.9E-06	0.955	589	0.437	531	1.000	1474	0.087	4043	0.273	308	0.566	948	0.607	14,874	9.5E-05	498	0.245	492	0.216	1152	1.000
	16_*TTC37*	24,909	5.7E-07	0.956	589	0.676	531	0.727	1474	0.333	4043	1.000	308	0.169	948	0.780	14,874	1.6E-04	498	0.289	492	0.002	1152	0.669
	11_*DHX36*	24,909	8.4E-06	0.138	589	0.025	531	0.002	1474	0.141	4043	0.004	308	0.916	948	0.064	14,874	0.031	498	0.921	492	0.884	1152	0.800
	6_*CASP3*	24,909	9.2E-06	0.041	589	0.191	531	0.032	1474	0.009	4043	0.022	308	0.027	948	0.204	14,874	0.153	498	0.007	492	0.931	1152	0.085

Table 3.

Top significant SNPs (p≤10–7) in the meta-analysis of *DCDC2* no-*APOE* _E4 strata

		common variants								rare+ultra-rare variants					
	rs	**rs1340698**	**rs114941574**	**rs112854846**	**rs6933291**	**rs73394040**	**rs73394022**	**rs114540201**	**rs75359737**	**rs147661578**	**rs116394689**	**rs807711**	**rs73727536**	**rs150137064**	**rs73727537**
	bp	**24256726**	**24310169**	**24236194**	**24346573**	**24245058**	**24225761**	**24315294**	**24350002**	**24318524**	**24335865**	**24294560**	**24357033**	**24191780**	**24366667**
	A1/A2	**A/G**	**T/C**	**A/G**	**C/G**	**A/G**	**A/C**	**A/G**	**A/G**	**A/C**	**A/G**	**T/C**	**C/G**	**A/G**	**T/C**
Metal	N	24890	24897	24902	24856	24898	24903	24873	24829	24873	24877	24900	24883	24834	24883
	P_{meta}	1.3E-07	1.8E-07	1.9E-07	1.9E-07	2.2E-07	2.3E-07	2.4E-07	2.6E-07	0.002	0.004	0.012	0.017	0.032	0.041
	P_{het}	0.348	0.631	0.618	0.255	0.610	0.636	0.607	0.287	0.512	0.082	0.183	0.221	0.093	0.157
ADNI n=589	MAF	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.0084	0.0059	0.0051	0.0076	0.0067	0.0067
	B	−0.04	0.03	0.03	0.06	0.03	0.03	0.03	0.06	0.02	0.09	0.06	0.08	−0.07	0.08
	SE	0.02	0.03	0.02	0.03	0.02	0.02	0.03	0.03	0.04	0.05	0.05	0.04	0.05	0.05
	P	0.111	0.358	0.253	0.029	0.253	0.253	0.358	0.029	0.675	0.073	0.222	0.074	0.140	0.070
CHAP n=531	MAF	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.0066	0.0028	0.0028	0.0047	0.0066	0.0047
	B	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.02	−0.02	0.03	−0.02	0.00	−0.02
	SE	0.01	0.02	0.01	0.01	0.01	0.01	0.02	0.01	0.02	0.04	0.04	0.03	0.02	0.03
	P	0.157	0.155	0.157	0.062	0.157	0.157	0.155	0.073	0.347	0.585	0.415	0.515	0.975	0.515
LLFS n=1,474	MAF	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.0054	0.0017	0.0041	0.0024	0.0126	0.0024
	B	0.00	−0.01	−0.01	−0.01	−0.01	−0.01	−0.01	−0.01	−0.01	0.09	0.03	0.05	−0.03	0.05
	SE	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.05	0.03	0.04	0.02	0.04
	P	0.788	0.498	0.676	0.628	0.676	0.676	0.498	0.691	0.679	0.094	0.458	0.286	0.179	0.286
NACC n=4,043	MAF	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.0075	0.0043	0.0019	0.0047	0.0119	0.0046
	B	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	−0.02	0.00	−0.02	0.02	−0.01	0.01
	SE	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.02	0.03	0.02	0.01	0.02
	P	0.364	0.224	0.278	0.241	0.278	0.278	0.244	0.183	0.178	0.845	0.474	0.458	0.512	0.526
NIA-LOAD n=308	MAF	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.03	0.0065	0.0065	NA	0.0065	0.0097	0.0065
	B	0.01	0.01	0.02	−0.01	0.01	0.02	0.01	−0.01	−0.12	0.05	NA	0.05	0.04	0.05
	SE	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.06	0.06	NA	0.06	0.05	0.06
	P	0.775	0.673	0.540	0.782	0.673	0.540	0.673	0.774	0.038	0.370	NA	0.370	0.386	0.370

		common variants								rare+ultra-rare variants					
	rs	**rs1340698**	**rs114941574**	**rs112854846**	**rs6933291**	**rs73394040**	**rs73394022**	**rs114540201**	**rs75359737**	**rs147661578**	**rs116394689**	**rs807711**	**rs73727536**	**rs150137064**	**rs73727537**
	bp	**24256726**	**24310169**	**24236194**	**24346573**	**24245058**	**24225761**	**24315294**	**24350002**	**24318524**	**24335865**	**24294560**	**24357033**	**24191780**	**24366667**
	A1/A2	**A/G**	**T/C**	**A/G**	**C/G**	**A/G**	**A/C**	**A/G**	**A/G**	**A/C**	**A/G**	**T/C**	**C/G**	**A/G**	**T/C**
ROSMAP n=948	MAF	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.03	0.0053	0.0042	0.0016	0.0042	0.0127	0.0042
	B	−0.03	−0.02	−0.02	−0.02	−0.02	−0.02	−0.02	−0.02	0.01	0.06	−0.09	0.07	−0.04	0.07
	SE	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.03	0.03	0.05	0.03	0.02	0.03
	P	0.018	0.129	0.066	0.048	0.066	0.066	0.129	0.055	0.626	0.059	0.087	0.031	0.045	0.031
UKBB n=14,857	MAF	0.03	0.02	0.02	0.03	0.02	0.02	0.02	0.03	0.0049	0.0039	0.0025	0.0041	0.0100	0.0042
	B	0.01	0.02	0.01	0.01	0.01	0.01	0.02	0.01	−0.02	−0.01	0.01	−0.01	0.00	0.00
	SE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01
	P	1.4E-04	9.6E-05	1.6E-04	1.7E-04	1.7E-04	1.7E-04	8.3E-05	2.8E-04	0.057	0.291	0.479	0.560	0.603	0.850
WNHW n=498	MAF	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.0191	0.0050	0.0070	NA	NA	NA
	B	−0.03	−0.03	−0.03	−0.03	−0.03	−0.03	−0.03	−0.03	0.00	0.00	−0.02	NA	NA	NA
	SE	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	NA	NA	NA
	P	0.002	0.010	0.002	0.014	0.002	0.000	0.010	0.014	0.653	0.787	0.233	NA	NA	NA
WAA n=492	MAF	0.16	0.05	0.15	0.06	0.15	0.15	0.05	0.06	0.0007	0.0641	0.1606	0.0385	0.0020	0.0385
	B	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	−0.01	0.00	0.00	0.00	0.01	NA
	SE	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	NA
	P	0.153	0.052	0.151	0.058	0.152	0.155	0.052	0.038	0.032	0.057	0.166	0.038	0.003	NA
WCH N=1,151	MAF	0.09	0.03	0.08	0.04	0.08	0.09	0.03	0.04	0.0030	0.0196	0.0745	0.0192	0.0040	0.0192
	B	−0.01	−0.01	−0.01	0.00	−0.01	−0.01	−0.01	0.00	0.02	−0.01	−0.01	0.01	0.00	0.01
	SE	0.00	0.01	0.00	0.01	0.00	0.00	0.01	0.01	0.02	0.01	0.01	0.01	0.02	0.01
	P	0.040	0.314	0.066	0.686	0.061	0.074	0.471	0.627	0.490	0.580	0.172	0.323	0.911	0.323

Table 4.

Common SNP-based *DCDC2-APOE* epistasis models by study cohort.

Cohort	TEST	rs1340698			
		A1	N	B	P
ADNI	SNP	G	1,090	0.04	0.134
	E4	G	1,090	−0.07	1.7E-15
	SNP*ε4	G	1,090	−0.07	0.078
CHAP	SNP	G	696	0.00	0.919
	E4	G	696	−0.02	0.002
	SNP*ε4	G	696	0.00	0.908
LLFS	SNP	G	1,874	0.01	0.731
	E4	G	1,874	0.00	0.671
	SNP*ε4	G	1,874	0.03	0.514
NACC	SNP	G	6,774	0.01	0.376
	E4	G	6,774	−0.04	1.4E-25
	SNP*ε4	G	6,774	−0.01	0.382
NIA-LOAD	SNP	G	482	0.01	0.877
	E4	G	482	−0.03	0.007
	SNP*ε4	G	482	0.04	0.393
ROSMAP	SNP	G	1,265	−0.03	0.022
	E4	G	1,265	−0.03	8.6E-08
	SNP*ε4	G	1,265	−0.01	0.837
UKB	SNP	G	20,174	0.01	9.8E-05
	E4	G	20,174	0.00	0.529
	SNP*ε4	G	20,174	−0.01	0.097
WHICAP_NHW	SNP	G	619	−0.03	3.6E-04
	E4	G	619	0.00	0.383
	SNP*ε4	G	619	0.04	0.008
WHICAP_AfAm	SNP	G	741	0.00	0.519
	E4	G	741	0.00	0.461
	SNP*ε4	G	741	0.00	0.871
WHICAP_CH	SNP	G	1,529	0.00	0.220
	E4	G	1,529	−0.01	1.7E-05
	SNP*ε4	G	1,529	−0.01	0.452

Table 5.

Association of *DCDC2* mRNA levels with cognitive and pathological phenotypes in the ROSMAP cohort.

Trait	n	logFC	t	P	P_{adj}	FDR_{Padj}
Slope of global cognition	661	1.10	4.73	2.8E-06	7.4E-05	0.002
Slope of episodic memory	660	0.97	4.31	1.9E-05	3.8E-04	0.004
Neuronal neurofibrillary tangles	691	−0.06	−3.70	2.3E-04	0.003	0.021
Amyloid beta protein	692	−0.06	−3.26	0.001	0.008	0.042
Neurofibrillary tangle burden	698	−0.17	−3.32	0.001	0.009	0.038
Neuritic plaque burden	698	−0.13	−3.17	0.002	0.011	0.039
Pathological AD diagnosis	698	−0.11	−3.46	0.001	0.012	0.036
Global measure of pathology	698	−0.10	−2.88	0.004	0.024	0.063
Neuronal loss substantia nigra	696	−0.08	−2.97	0.003	0.026	0.061
Transactive response DNA binding protein	640	−0.05	−2.50	0.013	0.138	0.290
Pathologic diagnosis of Lewy body diseases	674	−0.04	−2.07	0.039	0.332	0.634
Diffuse plaque burden	698	−0.06	−1.47	0.142	0.455	0.796
Global Parkinsonian Summary Score	696	−0.03	−1.81	0.071	0.482	0.779
Arteriolosclerosis	692	−0.03	−1.37	0.173	0.665	0.998
Any distribution of α-synuclein	674	−0.06	−1.78	0.075	0.668	0.935
Gross cerebral infarctions	698	0.03	0.93	0.354	0.798	1.047
Micro cerebral infarctions	698	−0.03	−1.03	0.303	0.821	1.014
Cerebral amyloid angiopathy	683	−0.02	−0.71	0.481	0.875	1.021
Diagnosis of Parkinson	695	0.03	0.48	0.630	0.891	0.985
Hippocampal sclerosis	694	−0.04	−0.80	0.423	0.898	0.943
Cerebral Atherosclerosis	695	0.00	0.17	0.863	0.964	0.964